BLAST Basic Local Alignment Search Tool

- Your search parameters were adjusted to search for a short input sequence.

Edit and Resubmit Save Search Strategies Formatting options Download

Blast 2 sequences

SEQ ID NO: 8

Results for: lcl|55839 None(22bp) ▼

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID
    lcl|55839
Description
    None
Molecule type
    nucleic acid
Query Length
    22

Subject ID
    gi|1914699|emb|X98077.1|
Description
    Hepatitis B virus complete genome, wild type
Molecule type
    nucleic acid
Subject Length
    3215
Program
    BLASTN 2.2.22+ Citation

Reference
Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.
Other reports: Search Summary [Taxonomy reports]

Search Parameters

Program	blastn
Word size	7
Expect value	1000
Hitlist size	100
Match/Mismatch scores	1,-3
Gapcosts	5,2
Filter string	F
Genetic Code	1

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	1.37406	1.37406
K	0.710603	0.710603
H	1.30725	1.30725

## Results Statistics

Effective search space 48120

```
▓▓▓ Designing or Testing PCR Primers? Try your s
```

Graphic Summary

Distribution of 8 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.
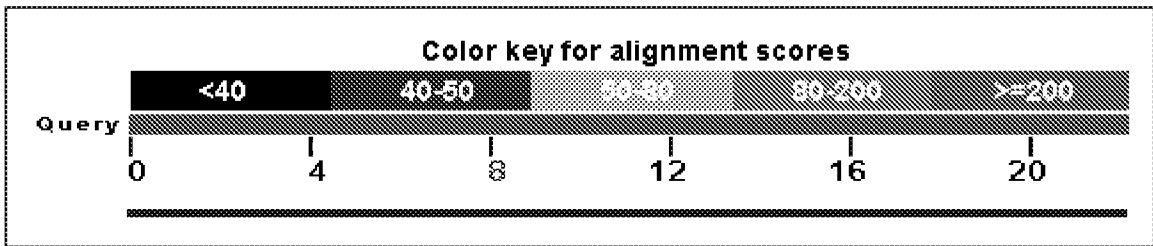
Dot Matrix View

Plot of lcl|55839 vs gi|1914699|emb|X98077.1| [?]

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.

Descriptions

Legend for links to other resources: 🔲 UniGene 🔲 GEO 🅶 Gene 🔲 Structure 🔲 Map Viewer

Sequences producing significant alignments:
(Click headers to sort columns)
```
X98077.1  Hepatitis B virus complete genome, wild type        44.1   148    100%   3e-09 100%
```

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Alignments Select All Get selected sequences Distance tree of results Multiple alignment NEW

>emb|X98077.1| Hepatitis B virus complete genome, wild type
Length=3215

Sort alignments for this subject seq
E value **Score Percent identity**
Query start position Subject star

 Score = 44.1 bits (22), Expect = 3e-09
 Identities = 22/22 (100%), Gaps = 0/22 (0%)
 Strand=Plus/Minus

Query 1   GGAGTCCGCGTAAAGAGAGGTG 22
            ||||||||||||||||||||||
Sbjct 1548 GGAGTCCGCGTAAAGAGAGGTG 1527

 Score = 16.4 bits (8), Expect = 0.58
 Identities = 8/8 (100%), Gaps = 0/8 (0%)
 Strand=Plus/Minus

Query 12   AAAGAGAG 19
            ||||||||
Sbjct 1953 AAAGAGAG 1946

 Score = 16.4 bits (8), Expect = 0.58
 Identities = 8/8 (100%), Gaps = 0/8 (0%)
 Strand=Plus/Plus

Query 12   AAAGAGAG 19
            ||||||||
Sbjct 2782 AAAGAGAG 2789

 Score = 14.4 bits (7), Expect = 2.3
 Identities = 7/7 (100%), Gaps = 0/7 (0%)
 Strand=Plus/Minus

Query 1   GGAGTCC 7
           |||||||
Sbjct 179 GGAGTCC 173

 Score = 14.4 bits (7), Expect = 2.3
 Identities = 7/7 (100%), Gaps = 0/7 (0%)
 Strand=Plus/Minus

Query 4   GTCCGCG 10
            |||||||
Sbjct 1455 GTCCGCG 1449

 Score = 14.4 bits (7), Expect = 2.3
 Identities = 7/7 (100%), Gaps = 0/7 (0%)
 Strand=Plus/Minus

Query 16   AGAGGTG 22
            |||||||
Sbjct 1598 AGAGGTG 1592

 Score = 14.4 bits (7), Expect = 2.3
 Identities = 7/7 (100%), Gaps = 0/7 (0%)

```
Strand=Plus/Minus

Query   16     AGAGGTG   22
               |||||||
Sbjct   1832   AGAGGTG   1826


 Score = 14.4 bits (7),  Expect = 2.3
 Identities = 7/7 (100%), Gaps = 0/7 (0%)
 Strand=Plus/Minus

Query   16     AGAGGTG   22
               |||||||
Sbjct   3182   AGAGGTG   3176
```

Select All Get selected sequences Distance tree of results Multiple alignment NEW